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1	AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA	59
	Met Pro	2
60	AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC	119
3	Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly His Gly His Ser Tyr Thr	22
120	ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC	179
23	Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu	42
180	ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT	239
43	Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu	62
240	CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG	299
63	His Val Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg	82
300	GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT	359
83	Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro Asn Ala Pro Pro	102
360	GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG	419
103	Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser Pro Pro Pro Tyr Ser Pro	118
420	AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC	479
480	ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC	539
540	AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA	599
600	TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA	659

FIG. 1

660 GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT 719

720 GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG 779

780 AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG 839

840 GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT 899

900 CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC 959

960 CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG 1019

1020 GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG 1079

1080 CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT 1139

1140 AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA 1199

1200 TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT 1259

1260 GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC 1319

1320 AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT 1379

1380 AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG 1439

1440 TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG 1499

1500 AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIG. 1 Continued

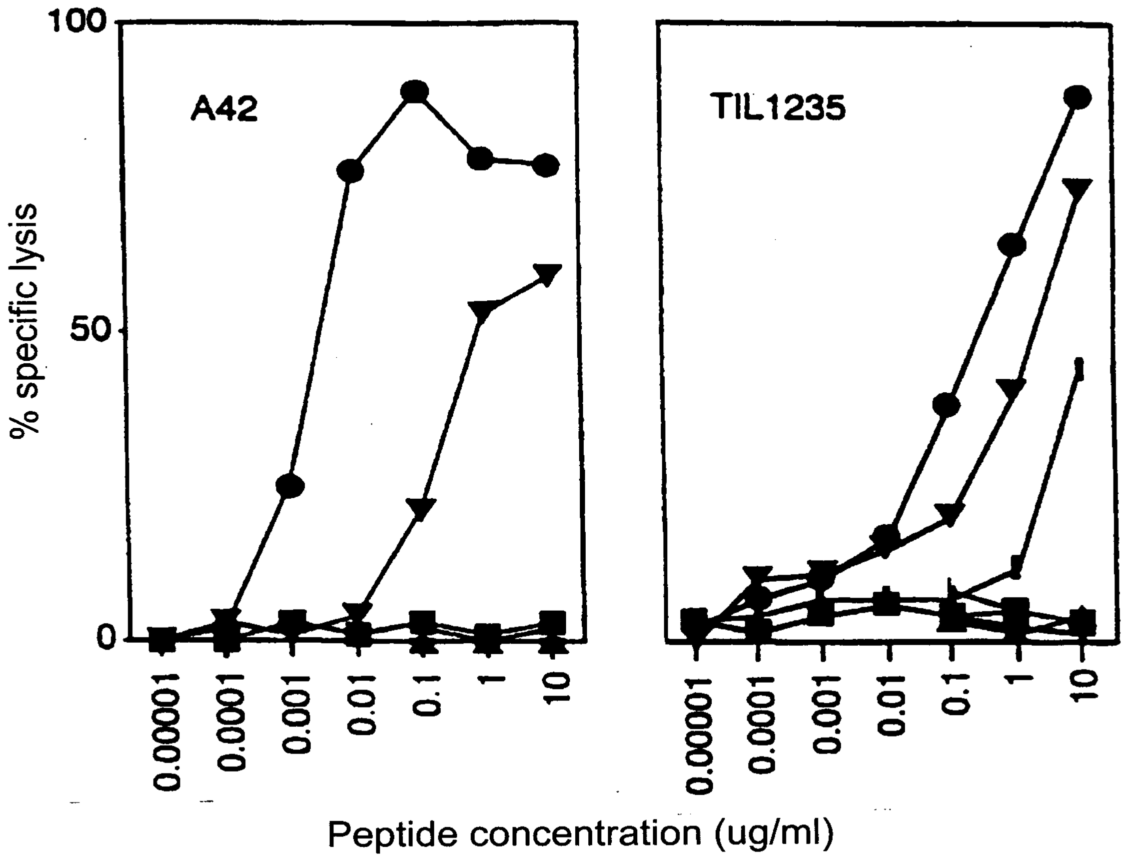
100
50
0
% specific lysis
A42
TIL1235
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2

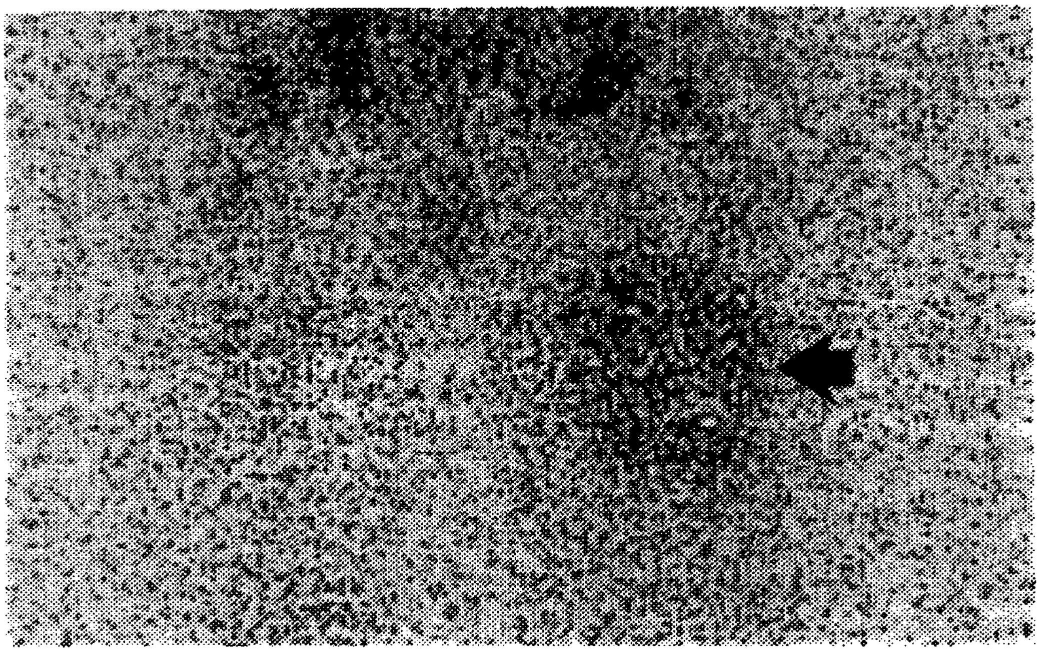

FIG. 3A

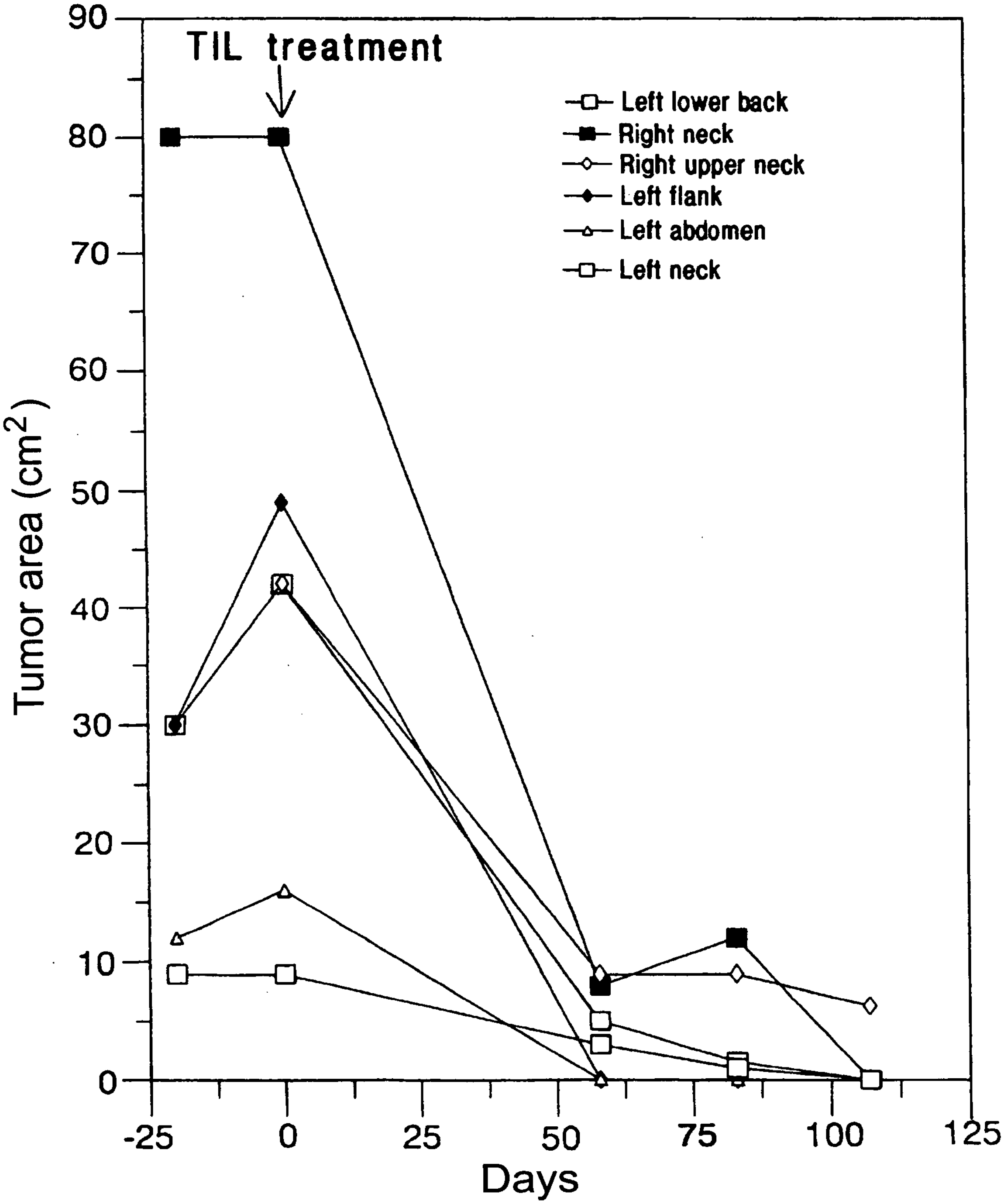
TIL treatment
Left lower back
Right neck
Right upper neck
Left flank
Left abdomen
Left neck
Tumor area (cm^2)
Days
90
80
70
60
50
40
30
20
10
0
-25
0
25
50
75
100
125

FIG. 3B

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIG. 4

```
TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG    1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA    1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC    1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA    1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG    1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC    1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG    1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA    1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG    1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA    1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG    1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC    1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG    1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC    1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG    1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC    1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG    1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG    1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG    1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC    1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC    1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC    2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG    2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC    2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT    2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA    2160
AAAAAAAAAA AA                                  2172
```

FIG. 4 (Continued)

```
  1  MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51  EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101  QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151  YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201  AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251  LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301  CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351  VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401  TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451  TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501  AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551  QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601  GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651  ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17     M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20       M-----V-----Q-----L----- ....-------------
gp100      M-----V-----Q-----L-----.....--------------
cDNA25FL   M-----F-----Q-----L-----.....--------------
cDNA25TR               Q-----L-----.........-----PPQWAAGLSTLI
           1     162   236   274   588         649
```

FIG. 5B

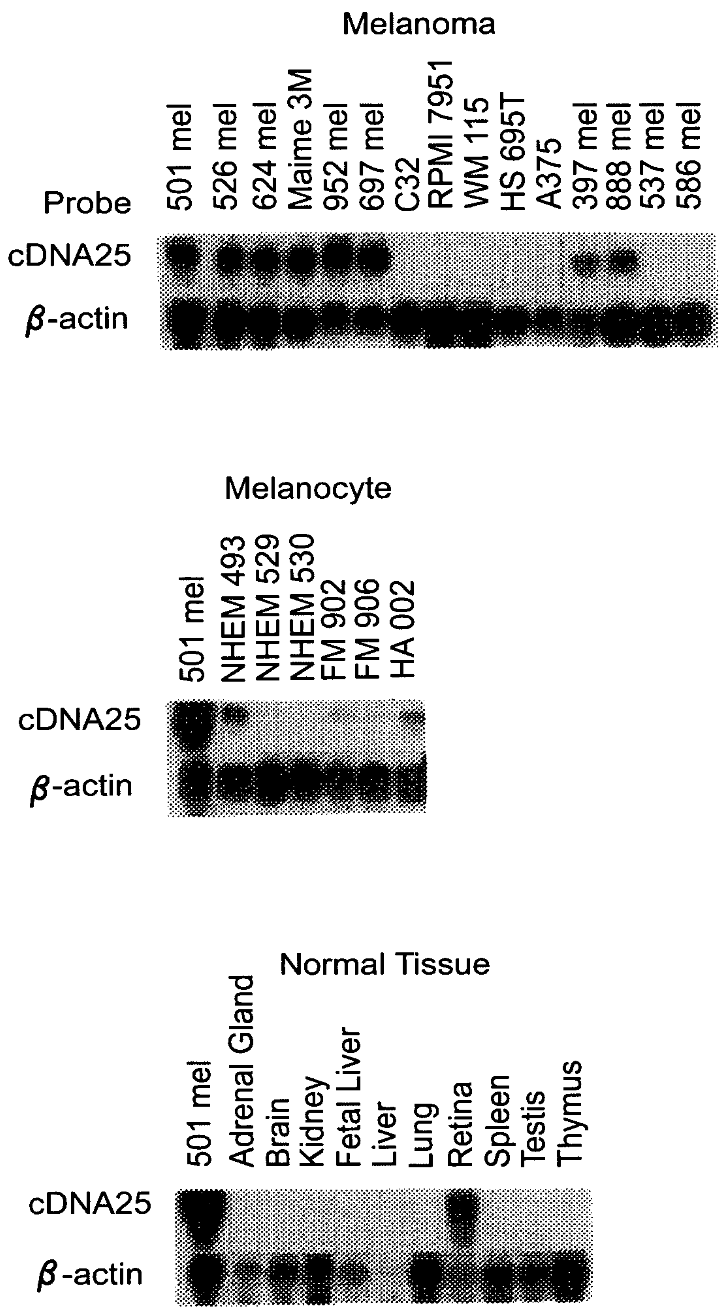
Melanoma
Probe
501 mel
526 mel
624 mel
Maime 3M
952 mel
697 mel
C32
RPMI 7951
WM 115
HS 695T
A375
397 mel
888 mel
537 mel
586 mel
cDNA25
β-actin
Melanocyte
501 mel
NHEM 493
NHEM 529
NHEM 530
FM 902
FM 906
HA 002
cDNA25
β-actin
Normal Tissue
501 mel
Adrenal Gland
Brain
Kidney
Fetal Liver
Liver
Lung
Retina
Spleen
Testis
Thymus
cDNA25
β-actin

FIG. 6